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RAW SEQUENCE LISTING   DATE: 02/19/2002
PATENT APPLICATION: US/09/677,822A   TIME: 14:47:44

Input Set : A:\GC527C2-seqlist.txt
Output Set: N:\CRF3\02192002\I677822A.raw

```
 3 <110> APPLICANT: Estell, David
 4        Harding, Fiona
 6 <120> TITLE OF INVENTION: PROTEINS PRODUCING AN ALTERED IMMUNOGENIC RESPONSE AND
 7        METHODS OF MAKING AND USING THE SAME
 9 <130> FILE REFERENCE: GC527C2
11 <140> CURRENT APPLICATION NUMBER: US 09/677,822A
12 <141> CURRENT FILING DATE: 2000-10-02
14 <150> PRIOR APPLICATION NUMBER: US 09/500,135
15 <151> PRIOR FILING DATE: 2000-02-08
17 <150> PRIOR APPLICATION NUMBER: US 09/060,872
18 <151> PRIOR FILING DATE: 1998-04-15
20 <160> NUMBER OF SEQ ID NOS: 240
22 <170> SOFTWARE: PatentIn Ver. 2.1
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 1495
26 <212> TYPE: DNA
27 <213> ORGANISM: Bacillus amyloliquefaciens
29 <220> FEATURE:
30 <221> NAME/KEY: mat_peptide
31 <222> LOCATION: (417)..(1495)
33 <220> FEATURE:
34 <221> NAME/KEY: CDS
35 <222> LOCATION: (96)..(1244)
37 <220> FEATURE:
38 <221> NAME/KEY: misc_feature
39 <222> LOCATION: (582)..(584)
40 <223> OTHER INFORMATION: The nnn at positions 582 through 584 which in a
41        preferred embodiment (aat) is to code for
42        asparagine, but which may also code for proline.
44 <220> FEATURE:
45 <221> NAME/KEY: misc_feature
46 <222> LOCATION: (585)..(587)
47 <223> OTHER INFORMATION: The nnn at positions 585 through 587 which in a
48        preferred embodiment (cct) is to code for proline,
49        but which may also code for asparagine.
51 <220> FEATURE:
52 <221> NAME/KEY: misc_feature
53 <222> LOCATION: (597)..(599)
54 <223> OTHER INFORMATION: The nnn at positions 597 to 599 which in a
55        preferred embodiment (aac) is to code for
56        asparagine, but which may also code for aspartic acid.
58 <220> FEATURE:
59 <221> NAME/KEY: misc_feature
```

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```
60  <222> LOCATION: (678)..(680)
61  <223> OTHER INFORMATION: The nnn at positions 678 through 680 which in a
62        preferred embodiment (gca) is to code for
63        alanine, but which may also code for serine.
65  <220> FEATURE:
66  <221> NAME/KEY: misc_feature
67  <222> LOCATION: (681)..(683)
68  <223> OTHER INFORMATION: The nnn at positions 681 through 683 which in a
69        preferred embodiment (tca) is to code for serine,
70        but which may also code for alanine.
72  <220> FEATURE:
73  <221> NAME/KEY: misc_feature
74  <222> LOCATION: (708)..(710)
75  <223> OTHER INFORMATION: The nnn at positions 708 through 710 which in a
76        preferred embodiment (gct) is to code for
77        alanine, but which may also code for aspartic acid.
79  <220> FEATURE:
80  <221> NAME/KEY: misc_feature
81  <222> LOCATION: (711)..(713)
82  <223> OTHER INFORMATION: The nnn at positions 711 through 713 which in a
83        preferred embodiment (gac) is to code for
84        aspartic acid, but which may also code for alanine.
86  <220> FEATURE:
87  <221> NAME/KEY: misc_feature
88  <222> LOCATION: (888)..(890)
89  <223> OTHER INFORMATION: The nnn at positions 888 through 890 which in a
90        preferred embodiment (act) is to code for
91        threonine, but which may also code for serine.
93  <220> FEATURE:
94  <221> NAME/KEY: misc_feature
95  <222> LOCATION: (891)..(893)
96  <223> OTHER INFORMATION: The nnn at positions 891 through 893 which in a
97        preferred embodiment (tcc) is to code for
98        serine, but which may also code for threonine.
100 <220> FEATURE:
101 <221> NAME/KEY: misc_feature
102 <222> LOCATION: (1167)..(1169)
103 <223> OTHER INFORMATION: The nnn at positions 1167 through 1169 which in
104       a preferred embodiment (gaa) is to code for
105       glutamic acid, but which may also code for glutamine.
107 <400> SEQUENCE: 1
108 ggtctactaa aatattattc catactatac aattaataca cagaataatc tgtctattgg  60
110 ttattctgca aatgaaaaaa aggagaggat aaaga atg aga ggc aaa aaa gta       113
111                                        Met Arg Gly Lys Lys Val
112                                                          -105
114 tgg atc agt ttg ctg ttt gct tta gcg tta atc ttt acg atg gcg ttc    161
115 Trp Ile Ser Leu Leu Phe Ala Leu Ala Leu Ile Phe Thr Met Ala Phe
116    -100               -95                 -90
118 ggc agc aca tcc tct gcc cag gcg gca ggg aaa tca aac ggg gaa aag    209
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119 Gly Ser Thr Ser Ser Ala Gln Ala Ala Gly Lys Ser Asn Gly Glu Lys
120 -85                 -80                 -75                 -70
122 aaa tat att gtc ggg ttt aaa cag aca atg agc acg atg agc gcc gct   257
123 Lys Tyr Ile Val Gly Phe Lys Gln Thr Met Ser Thr Met Ser Ala Ala
124                 -65                 -60                 -55
126 aag aag aaa gat gtc att tct gaa aaa ggc ggg aaa gtg caa aag caa   305
127 Lys Lys Lys Asp Val Ile Ser Glu Lys Gly Gly Lys Val Gln Lys Gln
128                 -50                 -45                 -40
130 ttc aaa tat gta gac gca gct tca gct aca tta aac gaa aaa gct gta   353
131 Phe Lys Tyr Val Asp Ala Ala Ser Ala Thr Leu Asn Glu Lys Ala Val
132         -35                 -30                 -25
134 aaa gaa ttg aaa aaa gac ccg agc gtc gct tac gtt gaa gaa gat cac   401
135 Lys Glu Leu Lys Lys Asp Pro Ser Val Ala Tyr Val Glu Glu Asp His
136     -20                 -15                 -10
138 gta gca cat gcg tac gcg cag tcc gtg cct tac ggc gta tca caa att   449
139 Val Ala His Ala Tyr Ala Gln Ser Val Pro Tyr Gly Val Ser Gln Ile
140  -5                 -1   1                 5                  10
142 aaa gcc cct gct ctg cac tct caa ggc tac act gga tca aat gtt aaa   497
143 Lys Ala Pro Ala Leu His Ser Gln Gly Tyr Thr Gly Ser Asn Val Lys
144             15                 20                 25
146 gta gcg gtt atc gac agc ggt atc gat tct tct cat cct gat tta aag   545
147 Val Ala Val Ile Asp Ser Gly Ile Asp Ser Ser His Pro Asp Leu Lys
148         30                 35                 40
150 gta gca ggc gga gcc agc atg gtt cct tct gaa aca nnn nnn ttc caa   593
151 Val Ala Gly Gly Ala Ser Met Val Pro Ser Glu Thr Xaa Xaa Phe Gln
152     45                 50                 55
154 gac nnn aac tct cac gga act cac gtt gcc ggc aca gtt gcg gct ctt   641
155 Asp Xaa Asn Ser His Gly Thr His Val Ala Gly Thr Val Ala Ala Leu
156  60                 65                 70                 75
158 aat aac tca atc ggt gta tta ggc gtt gcg cca agc nnn nnn ctt tac   689
159 Asn Asn Ser Ile Gly Val Leu Gly Val Ala Pro Ser Xaa Xaa Leu Tyr
160             80                 85                 90
162 gct gta aaa gtt ctc ggt nnn nnn ggt tcc ggc caa tac agc tgg atc   737
163 Ala Val Lys Val Leu Gly Xaa Xaa Gly Ser Gly Gln Tyr Ser Trp Ile
164         95                 100                105
166 att aac gga atc gag tgg gcg atc gca aac aat atg gac gtt att aac   785
167 Ile Asn Gly Ile Glu Trp Ala Ile Ala Asn Asn Met Asp Val Ile Asn
168             110                115                120
170 atg agc ctc ggc gga cct tct ggt tct gct gct tta aaa gcg gca gtt   833
171 Met Ser Leu Gly Gly Pro Ser Gly Ser Ala Ala Leu Lys Ala Ala Val
172     125                 130                135
174 gat aaa gcc gtt gca tcc ggc gtc gta gtc gtt gcg gca gcc ggt aac   881
175 Asp Lys Ala Val Ala Ser Gly Val Val Val Val Ala Ala Ala Gly Asn
176 140                 145                150                 155
178 gaa ggc nnn nnn ggc agc tca agc aca gtg ggc tac cct ggt aaa tac   929
179 Glu Gly Xaa Xaa Gly Ser Ser Ser Thr Val Gly Tyr Pro Gly Lys Tyr
180             160                165                170
182 cct tct gtc att gca gta ggc gct gtt gac agc agc aac caa aga gca   977
183 Pro Ser Val Ile Ala Val Gly Ala Val Asp Ser Ser Asn Gln Arg Ala
```

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184              175                 180                   185
186 tct ttc tca agc gta gga cct gag ctt gat gtc atg gca cct ggc gta   1025
187 Ser Phe Ser Ser Val Gly Pro Glu Leu Asp Val Met Ala Pro Gly Val
188              190                 195                   200
190 tct atc caa agc acg ctt cct gga aac aaa tac ggg gcg tac aac ggt   1073
191 Ser Ile Gln Ser Thr Leu Pro Gly Asn Lys Tyr Gly Ala Tyr Asn Gly
192              205                 210                   215
194 acg tca atg gca tct ccg cac gtt gcc gga gcg gct gct ttg att ctt   1121
195 Thr Ser Met Ala Ser Pro His Val Ala Gly Ala Ala Ala Leu Ile Leu
196 220                 225                 230                   235
198 tct aag cac ccg aac tgg aca aac act caa gtc cgc agc agt tta nnn   1169
199 Ser Lys His Pro Asn Trp Thr Asn Thr Gln Val Arg Ser Ser Leu Xaa
200              240                 245                   250
202 aac acc act aca aaa ctt ggt gat tct ttc tac tat gga aaa ggg ctg   1217
203 Asn Thr Thr Thr Lys Leu Gly Asp Ser Phe Tyr Tyr Gly Lys Gly Leu
204              255                 260                   265
206 atc aac gta cag gcg gca gct cag taa aacataaaaa accggccttg          1264
207 Ile Asn Val Gln Ala Ala Ala Gln
208              270                 275
210 gccccgccgg tttttttatt tttcttcctc cgcatgttca atccgctcca taatcgacgg 1324
212 atggctccct ctgaaaattt taacgagaaa cggcgggttg acccggctca gtcccgtaac 1384
214 ggccaagtcc tgaaacgtct caatcgccgc ttcccggttt ccggtcagct caatgccgta 1444
216 acggtcggcg gcgttttcct gataccggga gacggcattc gtaatcggat c          1495
219 <210> SEQ ID NO: 2
220 <211> LENGTH: 382
221 <212> TYPE: PRT
222 <213> ORGANISM: Bacillus amyloliquefaciens
224 <220> FEATURE:
225 <221> NAME/KEY: VARIANT
226 <222> LOCATION: (163)...(163)
227 <223> OTHER INFORMATION: Xaa = Asn or Pro
229 <220> FEATURE:
230 <221> NAME/KEY: VARIANT
231 <222> LOCATION: (164)...(164)
232 <223> OTHER INFORMATION: Xaa = Pro or Asn
234 <220> FEATURE:
235 <221> NAME/KEY: VARIANT
236 <222> LOCATION: (168)...(168)
237 <223> OTHER INFORMATION: Xaa = Asn or Asp
239 <220> FEATURE:
240 <221> NAME/KEY: VARIANT
241 <222> LOCATION: (195)...(195)
242 <223> OTHER INFORMATION: Xaa = Ala or Ser
244 <220> FEATURE:
245 <221> NAME/KEY: VARIANT
246 <222> LOCATION: (196)...(196)
247 <223> OTHER INFORMATION: Xaa = Ser or Ala
249 <220> FEATURE:
250 <221> NAME/KEY: VARIANT
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Output Set: N:\CRF3\02192002\I677822A.raw

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251 <222> LOCATION: (205)...(205)
252 <223> OTHER INFORMATION: Xaa = Ala or Asp
254 <220> FEATURE:
255 <221> NAME/KEY: VARIANT
256 <222> LOCATION: (206)...(206)
257 <223> OTHER INFORMATION: Xaa = Asp or Ala
259 <220> FEATURE:
260 <221> NAME/KEY: VARIANT
261 <222> LOCATION: (265)...(265)
262 <223> OTHER INFORMATION: Xaa = Thr or Ser
264 <220> FEATURE:
265 <221> NAME/KEY: VARIANT
266 <222> LOCATION: (266)...(266)
267 <223> OTHER INFORMATION: Xaa = Ser or Thr
269 <220> FEATURE:
270 <221> NAME/KEY: VARIANT
271 <222> LOCATION: (358)...(358)
272 <223> OTHER INFORMATION: Xaa = Gln or Glu
274 <400> SEQUENCE: 2
275 Met Arg Gly Lys Lys Val Trp Ile Ser Leu Leu Phe Ala Leu Ala Leu
276  1               5                  10              15
277 Ile Phe Thr Met Ala Phe Gly Ser Thr Ser Ser Ala Gln Ala Ala Gly
278              20              25                  30
279 Lys Ser Asn Gly Glu Lys Lys Tyr Ile Val Gly Phe Lys Gln Thr Met
280          35              40                  45
281 Ser Thr Met Ser Ala Ala Lys Lys Lys Asp Val Ile Ser Glu Lys Gly
282          50              55                  60
283 Gly Lys Val Gln Lys Gln Phe Lys Tyr Val Asp Ala Ala Ser Ala Thr
284  65              70              75                  80
285 Leu Asn Glu Lys Ala Val Lys Glu Leu Lys Lys Asp Pro Ser Val Ala
286              85              90                  95
287 Tyr Val Glu Glu Asp His Val Ala His Ala Tyr Ala Gln Ser Val Pro
288              100             105                 110
289 Tyr Gly Val Ser Gln Ile Lys Ala Pro Ala Leu His Ser Gln Gly Tyr
290          115             120                 125
291 Thr Gly Ser Asn Val Lys Val Ala Val Ile Asp Ser Gly Ile Asp Ser
292          130             135             140
293 Ser His Pro Asp Leu Lys Val Ala Gly Gly Ala Ser Met Val Pro Ser
294 145             150             155                 160
295 Glu Thr Xaa Xaa Phe Gln Asp Xaa Asn Ser His Gly Thr His Val Ala
296              165             170                 175
297 Gly Thr Val Ala Ala Leu Asn Asn Ser Ile Gly Val Leu Gly Val Ala
298          180             185                 190
299 Pro Ser Xaa Xaa Leu Tyr Ala Val Lys Val Leu Gly Xaa Xaa Gly Ser
300          195             200             205
301 Gly Gln Tyr Ser Trp Ile Ile Asn Gly Ile Glu Trp Ala Ile Ala Asn
302          210             215             220
303 Asn Met Asp Val Ile Asn Met Ser Leu Gly Gly Pro Ser Gly Ser Ala
304 225             230             235                 240
```

W--> (line 295)
W--> (line 299)

VERIFICATION SUMMARY   DATE: 02/19/2002
PATENT APPLICATION: US/09/677,822A   TIME: 14:47:45

Input Set : **A:\GC527C2-seqlist.txt**
Output Set: **N:\CRF3\02192002\I677822A.raw**

```
L:150 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:151 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:154 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:155 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:158 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:159 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:162 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:163 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:178 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:179 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:198 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:199 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:295 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:299 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:307 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:319 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
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